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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/029,495

DATE: 01/15/2002
TIME: 07:56:30

Input Set : A:\35905A.txt
Output Set: N:\CRF3\01152002\J029495.raw

3 <110> APPLICANT: Drmanac, Radoje T.
4 Labat, Ivan
5 Stache-Crain, Birgit
6 Dickson, Mark C.
7 Jones, Lee William
8 Ballinger, Dennis G.
9 Xue, Aidong
10 Tang, Y. Tom
11 Liu, Chenghua
12 Asundi, Vinod
14 <120> TITLE OF INVENTION: STEM CELL MAINTENANCE FACTOR MATERIALS AND METHODS
16 <130> FILE REFERENCE: 28110/35905A

ENTERED

18 <140> CURRENT APPLICATION NUMBER: US/10/029,495

19 <141> CURRENT FILING DATE: 2001-10-26

21 <150> PRIOR APPLICATION NUMBER: 09/378,667

22 <151> PRIOR FILING DATE: 1999-08-20

24 <150> PRIOR APPLICATION NUMBER: 09/687,527

25 <151> PRIOR FILING DATE: 2000-10-12

27 <160> NUMBER OF SEQ ID NOS: 13

29 <170> SOFTWARE: PatentIn Ver. 2.0

31 <210> SEQ ID NO: 1

32 <211> LENGTH: 560

33 <212> TYPE: DNA

34 <213> ORGANISM: Homo sapiens

36 <220> FEATURE:

37 <221> NAME/KEY: CDS

38 <222> LOCATION: (2)..(559)

40 <220> FEATURE:

41 <223> OTHER INFORMATION: hiwi-Hy/CG 389

43 <400> SEQUENCE: 1

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46 1 5 10 15

48 gtg stt gct cgg acc ttg aat aaa cag ggc atg atg atg agt atc gcc 97

W--> 49 Val Xaa Ala Arg Thr Leu Asn Lys Gln Gly Met Met Met Ser Ile Ala

50 20 25 30

52 acc aag atc gct atg cag atg act tgc aag ctc gga ggc gag ctg tgg 145

53 Thr Lys Ile Ala Met Gln Met Thr Cys Lys Leu Gly Gly Glu Leu Trp

54 35 40 45

56 gct gtg gaa ata cct tta aag tcc ctg atg gtg gtc ggt att gat gtc 193

57 Ala Val Glu Ile Pro Leu Lys Ser Leu Met Val Val Gly Ile Asp Val

58 50 55 60

60 tgt aaa gat gca ctc agc aag gac gtg atg gtt ggt att gat gtc 241

61 Cys Lys Asp Ala Leu Ser Lys Asp Val Met Val Val Gly Cys Val Ala

62 65 70 75 80

66 aqt gtt aac ccc aga atc acc agg tqq ttt tcc cgc tgt atc ctt cag 289

67 Ser Val Asn Pro Arg Ile Thr Arg Trp Phe Ser Arg Cys Ile Leu Gln

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68	85	90	95	
70	aga aca atg act gat gtt gca qat tgc ttg aaa gtt ttc atg act qga			337
71	Arg Thr Met Thr Asp Val Ala Asp Cys Leu Lys Val Phe Met Thr Gly			
72	100	105	110	
74	gca ctc aac aaa tgg tac aag tac aat cat gat ttg cca gca cgg ata			385
75	Ala Leu Asn Lys Trp Tyr Lys Tyr Asn His Asp Leu Pro Ala Arg Ile			
76	115	120	125	
78	att gtg tac cgt gct ggt gta ggg gat ggt cag ctg aaa aca ctt att			433
79	Ile Val Tyr Arg Ala Gly Val Gly Asp Gly Gln Leu Lys Thr Leu Ile			
80	130	135	140	
82	gaa tat gaa gtc cca caq ctg ctg agc agt gtg gca gaa tcc agc tca			481
83	Glu Tyr Glu Val Pro Gln Leu Leu Ser Ser Val Ala Glu Ser Ser Ser			
84	145	150	155	160
86	aat acc agc tca aga ctg tcg gtg att gtg gtc agg aag aag tgc atg			529
87	Asn Thr Ser Ser Arg Leu Ser Val Ile Val Val Arg Lys Lys Cys Met			
88	165	170	175	
90	cca cga ttc ttt acc gaa atg aac cgc act g			560
91	Pro Arg Phe Phe Thr Glu Met Asn Arg Thr			
92	180	185		
95	<210> SEQ ID NO: 2			
96	<211> LENGTH: 186			
97	<212> TYPE: PRT			
98	<213> ORGANISM: Homo sapiens			
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101	<221> NAME/KEY: SITE			
102	<222> LOCATION: (8)			
103	<223> OTHER INFORMATION: Xaa = Leu			
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106	<221> NAME/KEY: SITE			
107	<222> LOCATION: (9)			
108	<223> OTHER INFORMATION: Xaa = Asp or Tyr			
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111	<221> NAME/KEY: SITE			
112	<222> LOCATION: (18)			
113	<223> OTHER INFORMATION: Xaa = Leu or Val			
115	<400> SEQUENCE: 2			
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117	1	5	10	15
119	Val Xaa Ala Arg Thr Leu Asn Lys Gln Gly Met Met Met Ser Ile Ala			
120	20	25	30	
122	Thr Lys Ile Ala Met Gln Met Thr Cys Lys Leu Gly Gly Glu Leu Trp			
123	35	40	45	
125	Ala Val Glu Ile Pro Leu Lys Ser Leu Met Val Val Gly Ile Asp Val			
126	50	55	60	
128	Cys Lys Asp Ala Leu Ser Lys Asp Val Met Val Val Gly Cys Val Ala			
129	65	70	75	80
131	Ser Val Asn Pro Arg Ile Thr Arg Trp Phe Ser Arg Cys Ile Leu Gln			
132	85	90	95	
134	Arg Thr Met Thr Asp Val Ala Asp Cys Leu Lys Val Phe Met Thr Gly			

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135	100	105	110
137	Ala Leu Asn Lys Trp Tyr Lys Tyr Asn His Asp Leu Pro Ala Arg Ile		
138	115	120	125
140	Ile Val Tyr Arg Ala Gly Val Gly Asp Gly Gln Leu Lys Thr Leu Ile		
141	130	135	140
144	Glu Tyr Glu Val Pro Gln Leu Leu Ser Ser Val Ala Glu Ser Ser Ser		
145	145	150	155
147	Asn Thr Ser Ser Arg Leu Ser Val Ile Val Val Arg Lys Lys Cys Met		
148	165	170	175
150	Pro Arg Phe Phe Thr Glu Met Asn Arg Thr		
151	180	185	
154	<210> SEQ ID NO: 3		
155	<211> LENGTH: 523		
156	<212> TYPE: PRT		
157	<213> ORGANISM: Homo sapiens		
159	<220> FEATURE:		
160	<223> OTHER INFORMATION: hiwi		
162	<400> SEQUENCE: 3		
163	Gly Val Ser Phe Leu Glu Tyr Tyr Arg Lys Gln Tyr Asn Gln Glu Ile		
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166	Thr Asp Leu Lys Gln Pro Val Leu Val Ser Gln Pro Lys Arg Arg Arg		
167	167	20	25
169	Gly Pro Gly Gly Thr Leu Pro Gly Pro Ala Met Leu Ile Pro Glu Leu		
170	170	35	40
172	Cys Tyr Leu Thr Gly Leu Thr Asp Lys Met Arg Asn Asp Phe Asn Val		
173	173	50	55
175	Met Lys Asp Leu Ala Val His Thr Arg Leu Thr Pro Glu Gln Arg Gln		
176	176	65	70
178	Arg Glu Val Gly Arg Leu Ile Asp Tyr Ile His Lys Asn Asp Asn Val		
179	179	85	90
181	Gln Arg Glu Leu Arg Asp Trp Gly Leu Ser Phe Asp Ser Asn Leu Leu		
182	182	100	105
184	Ser Phe Ser Gly Arg Ile Leu Gln Thr Glu Lys Ile His Gln Gly Gly		
185	185	115	120
187	Lys Thr Phe Asp Tyr Asn Pro Gln Phe Ala Asp Trp Ser Lys Glu Thr		
188	188	130	135
190	Arg Gly Ala Pro Leu Ile Ser Val Lys Pro Leu Asp Asn Trp Leu Leu		
191	191	145	150
193	Ile Tyr Thr Arg Arg Asn Tyr Glu Ala Ala Asn Ser Leu Ile Gln Asn		
194	194	165	170
196	Leu Phe Lys Val Thr Pro Ala Met Gly Met Gln Met Arg Lys Ala Ile		
197	197	180	185
199	Met Ile Glu Val Asp Asp Arg Thr Glu Ala Tyr Leu Arg Val Leu Gln		
200	200	195	200
202	Gln Lys Val Thr Ala Asp Thr Gln Ile Val Val Cys Leu Leu Ser Ser		
203	203	210	215
205	Asn Arg Lys Asp Lys Tyr Asp Ala Ile Lys Lys Tyr Leu Cys Thr Asp		
206	206	225	230
208	Cys Pro Thr Pro Ser Gln Cys Val Val Ala Arg Thr Leu Gly Lys Gln		

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DATE: 01/15/2002
TIME: 07:56 30

Input Set : A:\35905A.txt
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209	245	250	255
211 Gln Thr Val Met Ala Ile Ala Thr Lys Ile Ala Leu Gln Met Asn Cys			270
212	260	265	
214 Lys Met Gly Gly Glu Leu Trp Arg Val Asp Ile Pro Leu Lys Leu Val			
215	275	280	285
217 Met Ile Val Gly Ile Asp Cys Tyr His Asp Met Thr Ala Gly Arg Arg			
218	290	295	300
220 Ser Ile Ala Gly Phe Val Ala Ser Ile Asn Glu Gly Met Thr Arg Trp			
221	305	310	315
223 Phe Ser Arg Cys Ile Phe Gln Asp Arg Gly Gln Glu Leu Val Asp Gly			320
224	325	330	335
226 Leu Lys Val Cys Leu Gln Ala Ala Leu Arg Ala Trp Asn Ser Cys Asn			
227	340	345	350
229 Glu Tyr Met Pro Ser Arg Ile Ile Val Tyr Arg Asp Gly Val Gly Asp			
230	355	360	365
233 Gly Gln Leu Lys Thr Leu Val Asn Tyr Glu Val Pro Gln Phe Leu Asp			
234	370	375	380
236 Cys Leu Lys Ser Ile Gly Arg Gly Tyr Asn Pro Arg Leu Thr Val Ile			
237	385	390	395
239 Val Val Lys Lys Arg Val Asn Thr Arg Phe Phe Ala Gln Ser Gly Gly			400
240	405	410	415
242 Arg Leu Gln Asn Pro Leu Pro Gly Thr Val Ile Asp Val Glu Val Thr			
243	420	425	430
245 Arg Pro Glu Trp Tyr Asp Phe Phe Ile Val Ser Gln Ala Val Arg Ser			
246	435	440	445
248 Gly Ser Val Ser Pro Thr His Tyr Asn Val Ile Tyr Asp Asn Ser Gly			
249	450	455	460
251 Leu Lys Pro Asp His Ile Gln Arg Leu Thr Tyr Lys Leu Cys His Ile			
252	465	470	475
254 Tyr Tyr Asn Trp Pro Gly Val Ile Arg Val Pro Ala Pro Cys Gln Tyr			480
255	485	490	495
257 Ala His Lys Leu Ala Phe Leu Val Gly Gln Ser Ile His Arg Glu Pro			
258	500	505	510
260 Asn Leu Ser Leu Ser Asn Arg Leu Tyr Tyr Leu			
261	515	520	
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265 <211> LENGTH: 866			
266 <212> TYPE: PRT			
267 <213> ORGANISM: Drosophila			
269 <220> FEATURE:			
270 <223> OTHER INFORMATION: aubergine			
272 <400> SEQUENCE: 4			
273 Met Asn Leu Pro Pro Asn Pro Val Ile Ala Arg Gly Arg Gly Gly			
274	1	5	10
276 Arg Lys Pro Asn Asn Val Glu Ala Asn Arg Gly Phe Ala Pro Ser Leu			15
277	20	25	30
279 Gly Gln Lys Ser Asp Pro Ser His Ser Glu Gly Asn Gln Ala Ser Gly			
280	35	40	45
282 Gly Asn Gly Gly Gly Asp Ala Gln Val Gly Pro Ser Ile Glu Lys			

RAW SEQUENCE LISTING
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Input Set A:\35905A.txt
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283	50	55	60
285	Ser Ser Leu Ser Ala Val Gln Met His Lys Ser Glu Gly Asp Pro Arg		
286	65	70	75 80
288	Gly Ser Val Arg Gly Arg Arg Leu Ile Thr Asp Leu Val Tyr Ser Arg		
289	85	90	95
291	Pro Pro Gly Met Thr Ser Lys Lys Gly Val Val Gly Thr His Ile Thr		
292	100	105	110
294	Val Gln Ala Asn Tyr Phe Lys Val Leu Lys Arg Pro Asn Trp Thr Ile		
295	115	120	125
297	Tyr Gln Tyr Arg Val Asp Phe Thr Pro Asp Val Glu Ala Thr Arg Leu		
298	130	135	140
300	Arg Arg Ser Phe Leu Tyr Glu His Lys Gly Ile Leu Gly Gly Tyr Ile		
301	145	150	155 160
303	Phe Asp Gly Thr Asn Met Phe Cys Ile Asn Gln Phe Lys Ala Val Gln		
304	165	170	175
306	Asp Ser Pro Tyr Val Leu Glu Leu Val Thr Lys Ser Arg Ala Gly Glu		
307	180	185	190
309	Asn Ile Glu Ile Lys Ile Lys Ala Val Gly Ser Val Gln Ser Thr Asp		
310	195	200	205
312	Ala Glu Gln Phe Gln Val Leu Asn Leu Ile Leu Arg Arg Ala Met Glu		
313	210	215	220
315	Gly Leu Asp Leu Lys Leu Val Ser Arg Tyr Tyr Asp Pro Gln Ala		
316	225	230	235 240
318	Lys Ile Asn Leu Glu Asn Phe Arg Met Gln Leu Trp Pro Gly Tyr Gln		
319	245	250	255
321	Thr Ser Ile Arg Gln His Glu Asn Asp Ile Leu Leu Cys Ser Glu Ile		
322	260	265	270
324	Cys His Lys Val Met Arg Thr Glu Thr Leu Tyr Asn Ile Leu Ser Asp		
325	275	280	285
327	Ala Ile Arg Asp Ser Asp Asp Tyr Gln Ser Thr Phe Lys Arg Ala Val		
328	290	295	300
330	Met Gly Met Val Ile Leu Thr Asp Tyr Asn Asn Lys Thr Tyr Arg Ile		
331	305	310	315 320
333	Asp Asp Val Asp Phe Gln Ser Thr Pro Leu Cys Lys Phe Lys Thr Asn		
334	325	330	335
336	Asp Gly Glu Ile Ser Tyr Val Asp Tyr Tyr Lys Lys Arg Tyr Asn Ile		
337	340	345	350
339	Ile Ile Arg Asp Leu Lys Gln Pro Leu Val Met Ser Arg Pro Thr Asp		
340	355	360	365
343	Lys Asn Ile Arg Gly Gly Asn Asp Gln Ala Ile Met Ile Ile Pro Glu		
344	370	375	380
346	Leu Ala Arg Ala Thr Gly Met Thr Asp Ala Met Arg Ala Asp Phe Arg		
347	385	390	395 400
349	Thr Leu Arg Ala Met Ser Glu His Thr Arg Leu Asn Pro Asp Arg Arg		
350	405	410	415
352	Ile Glu Arg Leu Arg Met Phe Asn Lys Arg Leu Lys Ser Cys Lys Gln		
353	420	425	430
355	Ser Val Glu Thr Leu Lys Ser Trp Asn Ile Glu Leu Asp Ser Ala Leu		
356	435	440	445

VERIFICATION SUMMARY
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Output Set: N:\CRF3\01152002\J029495.raw

L 18 M 270 C Current Application Number differs. Replaced Current Application Number
L 19 M 271 C Current Filing Date differs. Replaced Current Filing Date
L 45 M 341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L 49 M 341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:116 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:119 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2